

AMENDMENTS TO THE SPECIFICATION

Please replace the sequence alignment table beginning on page 16, line 13, and bridging to page 18, line 34, with the following amended sequence alignment table:

Nucleic acid alignment for SEQ ID NOS. 1, 3, 5, 7, and 9:

1	CanA	(1)	GTGAAGTACACAACCTAGCTATAGCGGGTATTATTGCCCTCGGCTGCCGC	50
	CanB	(1)	GTGAAGCCTACGGCTAGCCCTGGCTGGTATCATTGCCCTCGGCTGCCGA	
	CanC	(1)	ATGAGGTACACGACCCTAGCTCTGGCCGGCATAGTGGCCTCGGCTGCCGC	
CanD_partial		(1)	-----	
CanE_partial		(1)	-----	
Consensus		(1)	TGA G AC C CTAGC T GC GG AT T GCCTCGGCTGCCG	
			51	100
	CanA	(51)	CCTCGCCCTCCTAGCAGGCTTCGCCACCAACCCAGAGCCCCCTCAACAGCT	
	CanB	(51)	CCTCGCCCTGCTAGCAGGCTTCGCCACCAACCCAGAGCCCCGCTCAACAGCT	
	CanC	(51)	CCTCGCCCTGCTAGCAGGCTTCGCCACGACCCAGAGCCCCGCTAAGCAGCT	
CanD_partial		(1)	-----	AGCT
CanE_partial		(1)	-----	AGCT
Consensus		(51)	CCTCGCCCT CTAGCAGGCTTCGCCAC ACCCAGAGCCC CT A CAGCT	
			101	150
	CanA	(101)	TCTACGCCACCGGTACAGCACAGCAGTAAGCGAGCCAATAGACGTAGAA	
	CanB	(101)	TCTACGCCACCGGCACAGCACAGCAGTAAGCGAGCCAATAGACGTAGAG	
	CanC	(101)	TCTACGCCACCGGCACAGCACAGCAGTAAGCGAGCCAATAGACGTAGAG	
CanD_partial		(5)	TCTACGCCACCGGCACAGCACAGCAGTAAGCGAGCCAATAGACGTGGTA	
CanE_partial		(5)	TCTACGCCACCGGCACAGCACAGCAGGCAACAAAGCGAGCCAATAGACGTTGTA	
Consensus		(101)	TCTACGCCACCGGCACAGCACAGCAGTAAGCGAGCCAATAGACGTAGAA	
			151	200
	CanA	(151)	AGCCACCT---CGGCAGCATAACCCCGCAGCCGGCACAGGGCAGTGA	
	CanB	(151)	AGCCACCT---CAGCAGCATAAGCCCTGCTGCTGGCGCACAGGGCAGCCA	
	CanC	(151)	AGCCACCTAGACAACACCATAAGCCCTGCTGCGGGTGCACAGGGCTACAA	
CanD_partial		(55)	AGCAGCCTCGGTACG---CTAAATACTGCCGCTGGTGCACAGGGTAAGCA	
CanE_partial		(55)	AGCAACCTAACACGCCATAAGCCCTGCTGCCGGCGCCAGGGCAGCGT	
Consensus		(151)	AGCCACCT CA CA CATAGCCCTGCTGCCGGCGCACAGGGCAGC A	
			201	250
	CanA	(198)	CGACATAGGTTACGCAATAGTGTGGATAAAGGACCAGGTCAATGATGAA	
	CanB	(198)	GGACATAGGCTACTCAACGTGACCGCCAAGGATCAAGTGAACGTGACAA	
	CanC	(201)	GGACATAGGCTACATTAAGATAACTAACCGAGCTAAAGTTAATGAA	
CanD_partial		(102)	GACGCTAGGAGACATAACATATATGCGCACAATGACGTGAACATAACAA	
CanE_partial		(105)	GGGCATAGGCACCATAACATAGAGAACAGACTGACGTGAACGTGTTGA	
Consensus		(201)	GGACATAGGCTACATAA AATA A CAAG AT A GTGAACGT ATAA	
			201	250
	CanA	(248)	AGCTGAAGGTGACCCCTGCGTAACGCTGAGCAGCTAAAGCCCTACTTCAAG	
	CanB	(248)	AGATAAAAGGTGACCCCTGGCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG	
	CanC	(251)	AGCTGAAGGTGACTCTCGCTAACGCCGAGCAGCTAAAGCCCTACTTCGAC	
CanD_partial		(152)	AGCTAAAGGTACCGCTTGTCAACGCTGCAAGCTAACGACCATACTTCAAG	
CanE_partial		(155)	AGCTGAAGATAAACCTCGCCAACGCTGAGCAGCTAAAGCCCTACTTCGAC	
Consensus		(251)	AGCTGAAGGTGACCCCT GCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG	
			301	350
	CanA	(298)	TACCTACAGATACAGATAACAAGCGGCTATGAGACGAACAGCACAGCTCT	
	CanB	(298)	TACCTACAGATAGTGTAAAGAGCG-----	
	CanC	(301)	TACCTACAGCTAGTACTCACAAGCAAC-----GCCAC	
CanD_partial		(202)	TACCTGATAATAAGCTAGTAAGCCT-----GGACAGC-AA	
CanE_partial		(205)	TACCTACAGATAGTGTAAAGAGCGT-----TGACAGC-AA	

Consensus	(301)	TACCTACAGATAGTGCTAA	AAGCG	ACAGC	A
		351		400	
CanA	(348)	AGGCAACTTCAGCGAGACCAAGGCTGTGATAAGCCTCGACAACCCCAGCG			
CanB	(323)	AGGTAGCTGA--CGAGATCAAGGCCGTATAAGCATAGACAAGCCTAGCG			
CanC	(333)	TGGCACCGACA---TGGTTAAGGCTGTGCTAAGCCTCGAGAAGCCTAGCG			
CanD_partial	(237)	CGGCAACGAGTCCGAGGAAAGGGCATGATAACTCTATGGAAGCCTTACG			
CanE_partial	(240)	CGAGATCAAGGCTG-----TGCTAAGCCTCGAGAAGGCCAGCG			
Consensus	(351)	GGCA C A CGAG	AAGGC	GTGATAAGCCTCGAGAAGCCTAGCG	
		401		450	
CanA	(398)	CCGTGATAGTACTAGACAAGGAGGATATAGCAGTGCTCTATCCGGACAAG			
CanB	(371)	CCGTCATAATACTAGACAGCCAGGA-----			
CanC	(380)	CAGTCATAATACTAGACAACGATGA-----			
CanD_partial	(287)	CCGTGATAATACTAGACCATGAAGA-----			
CanE_partial	(278)	CAGTCATAATACTGGACAACGAGGA-----			
Consensus	(401)	CCGTCAATAACTAGACAACGAGGA			
		451		500	
CanA	(448)	ACCGGTTACACAAACACTTCGATATGGGTACCCGGTGAACCTGACAAGAT			
canB	(396)	-----CTTCGACA-----G-----			
CanC	(405)	-----CTACGATA-----G-----			
canD_partial	(312)	-----TTTCAACAACGACA-----			
canE_partial	(303)	-----CTTCCAGGGCGGC-----			
Consensus	(451)	CTTCGA A G			
		501		550	
CanA	(498)	AATTGTCTACAACGAGACAAAGGCCAGTAGCTATACTGAACTTCAAGGCCT			
canB	(405)	-----CAACAACAGAGCAAAG--ATAAGGCCACTG-----CCT			
CanC	(414)	-----CACTAACAGATACAGCTA-AAGGTAGA--A-----G-CCT			
canD_partial	(326)	-----TCGACAATGACGGCAACAATGACGCCAAGATAAGGGTTGAGCCT			
canE_partial	(316)	-----GACAACCAGTGCCAGATAGACGCCACC-----GCCT			
Consensus	(501)	C ACAAC AG AAAG AGAAGC A A T A		GCCT	
		551		600	
CanA	(548)	TCTACGAGGCTAAGGAGGGTATGCTATTGACAGCCTGCCAGTGATATT			
canB	(437)	ACTACGAGGCTAAGGAGGGCATGCTATTGACAGCCTACCGCTAATATT			
CanC	(446)	ACTATGAGGCTAAGGAGGGCATGCTATTGACAGCCTACCGTAATACTG			
canD_partial	(371)	ACTATGAGGCTAAGGAGGGTATGCT-----			
canE_partial	(347)	ACTACGAGGCTAAGGAGGGTATGCTA-----			
Consensus	(551)	ACTACGAGGCTAAGGAGGGTATGCTATTGACAGCCT CC T ATA T			
		601		642	
CanA	(598)	AACTTCCAGGTGCTACAAGTAGGCTAA-----			
canB	(487)	AACATACAGGTGCTAACAGCTCAGCTAA-----			
CanC	(496)	AACTTCCAGGTACTGAGCGCCGCTTGCAGTCCTTGTTGGA			
canD_partial	(396)	-----			
canE_partial	(373)	-----			
Consensus	(601)	AAC T CAGGT CT G T			

Amino Acid Alignment for SEQ ID NOS. 2, 4, 6, 8, and 10:

1		50			
CanA_pep	(1)	VKYTTLAIAGIIASAALALLAGFATTQSPNSFYATGTAQAVSEPIDVE			
CanB_pep	(1)	VKPTALALAGIIASAADLALLAGFATTQSPNSFYATGTAATSEPIDVE			
CanC_pep	(1)	MRYTTLALAGIVASAALALLAGFATTQSPNSFYATGTAQAVSEPIDVE			
CanD_partial	(1)	-----SFYATGTAQAVSEPIDVV			
CanE_partial	(1)	-----SFYATGTAEATSEPIDVV			
Consensus	(1)	VK T LALAGIIASAALALLAGFATTQSPNSFYATGTAQAVSEPIDVE			
		51		100	
CanA_pep	(51)	SHLG-SITPAAGAQGSDDIGYAIWIKDQVNDVVLKVTLRNAEQLKPYFK			
CanB_pep	(51)	SHLS-SIAPAAGAQGSQDIGYFNVTAKDQVNVTKIKVTLANAEQLKPYFK			
CanC_pep	(51)	SHLDNTIAPAAGAQGYKDMGYIKITNQSKVNVIKLKVTLANAEQLKPYFD			
CanD_partial	(19)	SSLGTINT-AAGAQGKQTLGDIYIYAHNDVNITKLKVTLANAAQLRPYFK			

CanE_partial	(19)	SNLNNTAIAPAAGAQGSVGIGSITIENKTDNVVVLKITLANAEQLKPYFD
Consensus	(51)	SHL SIAPAAGAQGS DIGYI I K VNVVVLKVTLANAEQLKPYFK
	101	
CanA_pep	(100)	YLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDK
CanB_pep	(100)	YLQIVLKVSEVAD-----EIKAVISIDKPSAVIILDSDQDFDSNNR--
CanC_pep	(101)	YLQLVITSNATG-----TDMVKAVLSLEKPSAVIILDNDDYDSTN--
CanD_partial	(68)	YLIKLVSLDSNG-----NESEEKGMITLWKPYAVIILDHEDFNNNDID--
CanE_partial	(69)	YLQIVLKVSDSN-----EIKAVLSLEKPSAVIILDNEDFQG-----
Consensus	(101)	YLQIVL S S EIKAVISLDKPSAVIILD EDF
	151	
CanA_pep	(150)	TGYTNNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGMLFDSPVIF
CanB_pep	(139)	-----AKISATAYYEAKEGMLFDSPVIF
CanC_pep	(141)	-----KIQ-----LKVEAYYEAKEGMLFDSPVIL
CanD_partial	(111)	-----N--DGNNDAKIRVVAYYEAKEGM-----
CanE_partial	(105)	-----GDNQCQIDATAYYEAKEGML-----
Consensus	(151)	A I AYYEAKEGMLFDSPVII
	201	214
CanA_pep	(200)	NFQVLQVG-----
CanB_pep	(163)	NIQVLSVS-----
CanC_pep	(166)	NFQVLSAACSPLW-
CanD_partial	(132)	-----
CanE_partial	(125)	-----
Consensus	(201)	N QVL